

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 11:42:22 Search time 56.329 seconds

(without alignments) 11410 644 Million cell updates/sec

Title: us-09-910-428-1

Perfect score: 26

Sequence: 1 ggtcctaattcttctgtaccag 26

Scoring table: IDENTITY NUC

Gapop 10 0 Gapext 1 0

Searches: 2054640 seqs 14551402878 positions 4100200

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 98

Maximum Match 100%

Listing first 45 summaries

Database: Genbank

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pl:*

10: gb_ro:*

11: gb_sl:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_ov:*

22: em_ov:*

23: em_pl:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sl:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_hum:*

32: em_htg_hum:*

33: em_htg_hum:*

34: em_htg_hum:*

35: em_htg_hum:*

36: em_htg_hum:*

37: em_htg_hum:*

38: em_sy:*

39: em_htg_hum:*

40: em_htg_hum:*

41: em_htg_hum:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DR	ID	Description
1	26	100.0	349	4	AF126288	AF126288 Bos tauru
2	26	100.0	732	4	AF040955	AF040955 Bos indic
3	26	100.0	25688	4	BT015741	BT015741 Bos tauru
4	19.8	76.2	126837	9	AL451106	AL451106 Human DNA
5	19.6	75.4	144427	2	AC094612	AC094612 Rattus no
6	19.6	75.4	133521	2	AC126814	AC126814 Rattus no
7	19.6	75.4	196524	2	AC101881	AC101881 Mus muscu
8	19.4	74.6	51881	9	AL158049	AL158049 Human DNA
9	19.2	73.8	115297	2	U812207	U812207 Homo sapien
10	19.2	73.8	153909	2	AC124782	AC124782 Rattus no
11	19.2	73.8	156042	2	AC125295	AC125295 Rattus no
12	19.2	73.8	156091	9	AC092422	AC092422 Human chr
13	19.2	72.8	147776	9	AL592546	AL592546 Human chr
14	19.2	73.8	187357	2	AC129388	AC129388 Rattus no
15	19.2	73.8	193446	2	AC094597	AC094597 Rattus no
16	18.8	72.3	80324	2	AC119858	AC119858 Mus muscu
17	18.8	72.3	121448	9	AC092699	AC092699 Homo sapi
18	18.8	72.3	155123	2	AC129447	AC129447 Rattus no
19	18.8	72.3	163236	2	AC095804	AC095804 Rattus no
20	18.8	72.3	163236	2	AC129447	AC129447 Rattus no
21	18.8	72.3	163236	2	AC129447	AC129447 Rattus no
22	18.8	72.3	163236	2	AC129447	AC129447 Rattus no
23	18.8	72.3	163236	2	AC129447	AC129447 Rattus no
24	18.8	72.3	163236	2	AC129447	AC129447 Rattus no
25	18.8	72.3	163236	2	AC129447	AC129447 Rattus no
26	18.8	72.3	163236	2	AC129447	AC129447 Rattus no
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28	18.6	71.5	588	4	BT015741	BT015741 Bos tauru
29	18.6	71.5	588	4	BT015741	BT015741 Bos tauru
30	18.6	71.5	588	4	BT015741	BT015741 Bos tauru
31	18.6	71.5	588	4	BT015741	BT015741 Bos tauru
32	18.6	71.5	588	4	BT015741	BT015741 Bos tauru
33	18.6	71.5	588	4	BT015741	BT015741 Bos tauru
34	18.6	71.5	588	4	BT015741	BT015741 Bos tauru
35	18.6	71.5	588	4	BT015741	BT015741 Bos tauru
36	18.6	71.5	588	4	BT015741	BT015741 Bos tauru
37	18.6	71.5	588	4	BT015741	BT015741 Bos tauru
38	18.6	71.5	588	4	BT015741	BT015741 Bos tauru
39	18.6	71.5	588	4	BT015741	BT015741 Bos tauru
40	18.6	71.5	588	4	BT015741	BT015741 Bos tauru
41	18.6	71.5	588	4	BT015741	BT015741 Bos tauru
42	18.6	71.5	588	4	BT015741	BT015741 Bos tauru
43	18.6	71.5	588	4	BT015741	BT015741 Bos tauru
44	18.6	71.5	588	4	BT015741	BT015741 Bos tauru
45	18.6	71.5	588	4	BT015741	BT015741 Bos tauru

ALIGNMENTS

RESULT 1

LOCUS AF126288 349 bp DNA linear MAY 27 1999

DEFINITION Bos taurus growth hormone receptor (GHR) gene, promoter and 5' untranslated region.

ACCESSION AF126288

VERSION AF126288.1 GI:4894683

KEYWORDS

SOURCE

ORGANISM

Bos taurus

Bos taurus

Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bos (bases 1 to 349)

REFERENCE

Ge M., Davis M.E., Hines H.C. and Ivins R.M.

Prod. No. is the number of results predicted by chance to have a

TITLE Two allelic DGE polymorphism detected in the promoter region of the bovine GHR gene
JOURNAL Anim. Genet. 30 (1), 71 (1999)
MEDLINE 99159203
PubMed 10050296
REFERENCE 2 (bases 1 to 349)
AUTHORS Ge, M., Davis, M.E., Hines, B.C. and Ivins, K.M.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-1999) Animal Sciences, The Ohio State University, 2027 Coffey Road Columbus, OH 43210, USA
FEATURES
source location/Qualifiers
1..349
/organism="Bos taurus"
/db_xref="taxon:9913"
/chromosome="20"
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149
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403..349
/gene="GHR"
/product="growth hormone receptor"
303..349
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403..349
5'UTR
BASE COUNT 77 a 72 c 106 g 94 t
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Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTAACTTTTCTGTGACAGG 26
DB 154 GTGCTAACTTTTCTGTGACAGG 179
RESULT 2
AF040955 732 bp DNA linear MAM 16-JAN-1998
LOCUS Bos indicus growth hormone receptor promoter and exon 1, partial
DEFINITION sequence.
ACCESSION AF040955
VERSION AF040955.1 GI:2773337
KEYWORDS
SOURCE Bos indicus.
ORGANISM Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovidae; Bos.
REFERENCE 1 (bases 1 to 732)
AUTHORS Lucy, M.C. and Boyd, C.K.
TITLE Promoter and first exon for bovine growth hormone receptor isolated from Bos indicus
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 732)
AUTHORS Lucy, M.C. and Boyd, C.K.
TITLE Direct Submission
JOURNAL Submitted (02-JAN-1998) Animal Sciences, University of Missouri, 164 ASRC, Columbia, MO 65211, USA
FEATURES
source location/Qualifiers
1..732
/organism="Bos indicus"
/strain="Hraham"
/db_xref="taxon:9915"
1..569
/note="growth hormone receptor promoter"

MRNA 570..2732
EXON /product="growth hormone receptor"
570..2732
BASE COUNT 176 a 168 c 175 g 213 t
ORIGIN
Query Match 100.0%; Score 26; DB 4; Length 732;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTAACTTTTCTGTGACAGG 26
DB 433 GTGCTAACTTTTCTGTGACAGG 458
RESULT 3
BT015731 25688 bp DNA linear MAM 04-SEP-2001
LOCUS Bos taurus somatotropin receptor gene, exon 1 and liver-specific
DEFINITION promoter region.
ACCESSION BT015731
VERSION BT015731.2 GI:13570031
KEYWORDS
SOURCE Bos taurus.
ORGANISM Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovidae; Bos.
REFERENCE 1 (bases 1 to 25688)
AUTHORS Heap, D., Lucy, M.C., Collier, K.J., Boyd, C.K. and Warren, M.C.
TITLE Rapid communication: nucleotide sequence of the promoter and first exon of the somatotropin receptor gene in cattle
JOURNAL J. Anim. Sci. 73 (5), 1529 (1995)
MEDLINE 95384696
REFERENCE 2 (bases 1 to 25688)
AUTHORS Lucy, M.C.
TITLE Direct Submission
JOURNAL Submitted (11-OCT-1994) Matthew C. Lucy, Animal Science, University of Missouri, 164 Animal Science Research Center, Columbia, MO 65211, USA
REFERENCE 3 (bases 1 to 25688)
AUTHORS Jiang, H. and Lucy, M.C.
TITLE Involvement of hepatocyte nuclear factor-4 in the expression of the growth hormone receptor 1A messenger RNA levels in bovine liver
JOURNAL Mol. Endocrinol. 15 (6), 1023-1034 (2001)
MEDLINE 21270340
COMMENT On Apr 10, 2001 this sequence version replaced gi:560024.
FEATURES
source location/Qualifiers
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/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="13-1"
/sex="male"
/tissue="liver"
9763..10256
/note="liver-specific"
10136..10175
/type="tandem"
10232..10237
/note="putative"
10257..25688
/product="growth hormone receptor"
10258..10465
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/number=1A
10258..10492
/note="growth hormone receptor; somatotropin receptor"
25660..25688
EXON

COMMENT

On Dec 20, 2001 this sequence version replaced g1:15624447.

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.bcm.tmc.edu>

Contact: basc_help@bcm.tmc.edu

Project information

Center project name: CHA

Center clone name: CH230-541

Summary Statistics

Assembly program: Phrap version 0.900320First call to findPrapList

Consensus quality: 133897 bases at least Q40

Consensus quality: 142583 bases at least Q30

Consensus quality: 148654 bases at least Q20

Estimated insert size: 135494; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; average ip estimation

Quality coverage: 2.1x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.bcm.tmc.edu/~basc/ftp/Phrap_data.html)

* NOTE: This is a 'working draft' sequence. It currently

* consists of 53 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

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1 9929: contig of 9929 bp in length
* 9930 10029: gap of unknown length
* 10030 19562: contig of 9533 bp in length
* 19563 19662: gap of unknown length
* 19663 25954: contig of 6292 bp in length
* 25955 26054: gap of unknown length
* 26055 31955: contig of 5900 bp in length
* 31955 32054: gap of unknown length
* 32055 38437: contig of 6382 bp in length
* 38437 38536: gap of unknown length
* 38537 42643: contig of 4107 bp in length
* 42644 42744: gap of unknown length
* 42744 47681: contig of 4938 bp in length
* 47682 47782: gap of unknown length
* 47782 51504: contig of 3723 bp in length
* 51505 51605: gap of unknown length
* 51605 54660: contig of 3056 bp in length
* 54661 54760: gap of unknown length
* 54761 59890: contig of 5130 bp in length
* 59891 59990: gap of unknown length
* 59991 63789: contig of 3699 bp in length
* 63790 66997: gap of unknown length
* 66998 67097: contig of 3208 bp in length
* 67098 70030: gap of unknown length
* 70031 70130: contig of 2933 bp in length
* 70131 74162: gap of unknown length
* 74163 74262: gap of unknown length
* 74263 77599: contig of 3337 bp in length
* 77600 77699: gap of unknown length
* 77700 79923: contig of 2224 bp in length
* 79924 80023: gap of unknown length
* 80024 82519: contig of 2596 bp in length
* 82520 82619: gap of unknown length
* 82620 85120: contig of 2371 bp in length
* 85121 88663: gap of unknown length
* 88664 88763: contig of 3543 bp in length
* 88764 91497: gap of unknown length
* 91498 91597: contig of 2734 bp in length
* 91598 93139: gap of unknown length
* 93140 93239: gap of unknown length
* 93240 95302: contig of 2063 bp in length
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* 95403 98048: contig of 4636 bp in length
* 98049 98148: gap of unknown length
* 98149 102199: contig of 4051 bp in length
* 102200 102299: gap of unknown length
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* 105345 105443: gap of unknown length
* 105444 108005: contig of 2562 bp in length
* 108006 108105: gap of unknown length
* 108106 109200: contig of 1715 bp in length
* 109201 109920: gap of unknown length
* 109921 109929: gap of unknown length
* 109930 112114: contig of 2094 bp in length
* 112115 112119: gap of unknown length
* 112120 114297: contig of 2183 bp in length
* 114298 114397: gap of unknown length
* 114398 116200: contig of 1803 bp in length
* 116201 116300: gap of unknown length
* 116301 118540: contig of 2240 bp in length
* 118541 118640: gap of unknown length
* 118641 120017: contig of 1377 bp in length
* 120018 120117: gap of unknown length
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* 121655 121754: gap of unknown length
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* 123049 123140: gap of unknown length
* 123141 125246: contig of 2106 bp in length
* 125247 125345: gap of unknown length
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* 127938 128037: gap of unknown length
* 128038 128965: contig of 1928 bp in length
* 128966 130065: gap of unknown length
* 130066 131785: contig of 1720 bp in length
* 131786 131885: gap of unknown length
* 131886 134325: contig of 2440 bp in length
* 134326 134425: gap of unknown length
* 134426 135449: contig of 1924 bp in length
* 135450 136449: gap of unknown length
* 136450 138224: contig of 1775 bp in length
* 138225 138324: gap of unknown length
* 138325 139939: contig of 1675 bp in length
* 140000 140099: gap of unknown length
* 140100 141317: contig of 1218 bp in length
* 141318 141417: gap of unknown length
* 141418 142711: contig of 1294 bp in length
* 142712 142811: gap of unknown length
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* 145119 146940: contig of 1822 bp in length
* 146941 147040: gap of unknown length
* 147041 148586: contig of 1546 bp in length
* 148587 148686: gap of unknown length
* 148687 149923: contig of 1237 bp in length
* 149924 150023: gap of unknown length
* 150024 151413: contig of 1390 bp in length
* 151414 151513: gap of unknown length
* 151514 152734: contig of 1221 bp in length
* 152735 152834: gap of unknown length
* 152835 153912: contig of 1078 bp in length
* 153913 154012: gap of unknown length
* 154013 156181: contig of 2169 bp in length
* 156182 156281: gap of unknown length
* 156282 157348: contig of 1067 bp in length
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* 157449 158469: contig of 1021 bp in length
* 158470 158569: gap of unknown length
* 158570 159681: contig of 1112 bp in length
* 159682 160789: gap of unknown length
* 160790 160889: contig of 1008 bp in length
* 160890 160989: gap of unknown length

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Query Match 75.4% Score 19.61 DB 2: Length 164427;
 Best Local Similarity 84.6% Pred. No. 1.7e+02;
 Matches 22: Conservative 0: Mismatches 4: Indels 0: Gaps 0:

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49297	51707	contig of 2411 bp in length
51708	51807	gap of unknown length
51808	54110	contig of 2303 bp in length
54111	54210	gap of unknown length
54211	57375	contig of 3165 bp in length
57376	57475	gap of unknown length
57476	60536	contig of 3061 bp in length
60537	60637	gap of unknown length
60638	63317	contig of 2681 bp in length
63318	63417	gap of unknown length
63418	65968	contig of 2551 bp in length
65969	66068	gap of unknown length
66069	69498	contig of 3430 bp in length
69499	71526	gap of unknown length
71527	71626	contig of 1928 bp in length
71627	74676	gap of unknown length
74677	74776	gap of unknown length
74777	77583	contig of 2807 bp in length
77584	77683	gap of unknown length
77684	80148	contig of 2465 bp in length
80149	80248	gap of unknown length
80249	82557	contig of 2393 bp in length
82558	82657	gap of unknown length
82658	84481	contig of 1824 bp in length
84482	87302	gap of unknown length
87303	87402	contig of 2721 bp in length
87403	90697	gap of unknown length
90698	90798	contig of 3295 bp in length
90799	93987	gap of unknown length
93988	94086	contig of 3189 bp in length
94087	97550	gap of unknown length
97551	97650	contig of 3464 bp in length
97651	102172	gap of unknown length
102173	102272	contig of 4522 bp in length
102273	105168	gap of unknown length
105169	105268	contig of 2896 bp in length
105269	109192	gap of unknown length
109193	109292	contig of 3924 bp in length
109293	114339	gap of unknown length
114340	114439	contig of 5047 bp in length
114440	118107	gap of unknown length
118108	118207	contig of 3668 bp in length
118208	123652	gap of unknown length
123653	123752	contig of 4445 bp in length
123753	128324	gap of unknown length
128325	128424	contig of 5572 bp in length
128425	133512	gap of unknown length
133513	133612	contig of 5088 bp in length
133613	141318	gap of unknown length
141319	141418	contig of 7706 bp in length
141419	147572	gap of unknown length
147573	147672	contig of 6154 bp in length
147673	155647	gap of unknown length
155648	155747	contig of 7975 bp in length
155748	163030	gap of unknown length
163031	163130	contig of 7283 bp in length
163131	173435	gap of unknown length
173436	173535	contig of 10305 bp in length

AC101881	194624 bp	DNA	Submitted 21-Aug-2002
DEFINITION	Mus musculus clone H423-387F19, WORKING DRAFT SEQUENCE, 8 unordered pieces.		
AC101881	3122381426		
AC101881.2	3122381426		
VERSION	HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.		
KEYWORDS	house mouse.		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
REFERENCE	1 (bases 1 to 194624)		
AUTHORS	Britten, B., Nussbaum, C. and Lander, E.		
TITLE	Mus musculus, clone RP23-387F19		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 194624)		
AUTHORS	Britten, B., Lincoln, L., Nussbaum, C., Lander, E., Allen, N., Anderson, S., Barina, N., Bastien, V., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campoliano, A., Chang, J., Charzart, B., Choquet, Y., Colangelo, M., Collins, S., Collum, A., Cook, A., Cooke, P., D'Alessandro, K., Davis, K., Diaz, J., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Garbino, S., Grinde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heald, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kelly, C., Lakocque, K., Lamazares, E., Landers, T., Lebecky, J., Levine, R., Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McKean, P., McKernan, K., McPheeters, R., Meldrum, J., Meneses, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Rector, R., Rieback, M., Riley, R., Risc, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, H., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testa, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trilling, J., Vassiliev, H., Vel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zehnke, L., Ziemer, A. and Zody, M.		
TITLE	Direct Submission		
JOURNAL	Submitted (43-Nov-2001) Whitehead Institute/MIT Center for Genome Research, 330 Charles Street, Cambridge, MA 02141, USA		
REFERENCE	3 (bases 1 to 194624)		
AUTHORS	Britten, B., Nussbaum, C., Lander, E., Allen, N., Anderson, S., Barina, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, H., Camarata, J., Chang, J., Charzart, B., Choquet, Y., Collum, A., Cook, A., Cooke, P., D'Alessandro, K., Davis, K., Diaz, J., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Garbino, S., Grinde, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kelly, C., Lakocque, K., Lamazares, E., Landers, T., Lebecky, J., Levine, R., Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McKean, P., McKernan, K., McPheeters, R., Meldrum, J., Meneses, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Rector, R., Rieback, M., Riley, R., Risc, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, H., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testa, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trilling, J., Vassiliev, H., Vel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zehnke, L., Ziemer, A. and Zody, M.		
TITLE	Direct Submission		
JOURNAL	Submitted (43-Nov-2001) Whitehead Institute/MIT Center for Genome Research, 330 Charles Street, Cambridge, MA 02141, USA		
COMMENT	On Aug 21, 2002 this sequence version replaced 17060657. All releases were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.gcc.washington.edu/pub/wrapmaster.html		

Query Match Similarity 75.44: Score 19.6: PR 2: Length 183621:
 Best Local 22: Conservative 0, Mismatches 4, Indels 0, Gaps 0:
 Matches 22: Conservative 0, Mismatches 4, Indels 0, Gaps 0:

DB 80065 575-TTAACTTCTGATCAG 80040
 AC101881/c

Center: Whitehead Institute/MIT Center for Genome Research
 Center code: W1B8
 Web site: http://www.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 Project information
 Center project name: L17690

[illegible]

JOURNAL
 2 (bases 1 to 156942)
 REFERENCE
 Morley K C
 TITLE
 Direct Submission
 Submitted (22-Nov-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 156942)
 REFERENCE
 Morley K C
 TITLE
 Direct Submission
 Submitted (11-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

COMMENT

Center: Baylor College of Medicine
 Center code: BCM
 Web Site: <http://www.hgsc.bcm.tmc.edu>
 Contact: hgsc-help@bcm.tmc.edu
 Project Information
 Center project name: GDBT
 Center clone name: CH230-9A11

Summary Statistics

Sequencing vector: plasmid;
 Chemistry: dye terminator Big Dye, 100% of reads
 Assembly program: phrap; version 0.990329
 Consensus quality: 110586 bases at least Q40
 Consensus quality: 115829 bases at least Q30
 Consensus quality: 119348 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/hgsc/submit_data.html)
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 59 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1007: contig of 1007 bp in length
 * 1008 1107: gap of unknown length
 * 1109 2347: contig of 1240 bp in length
 * 2348 2447: gap of unknown length
 * 2449 3631: contig of 1184 bp in length
 * 3632 3731: gap of unknown length
 * 3732 4971: contig of 1240 bp in length
 * 4972 5071: gap of unknown length
 * 5072 6292: contig of 1221 bp in length
 * 6293 6392: gap of unknown length
 * 6393 8135: contig of 1743 bp in length
 * 8136 8235: gap of unknown length
 * 8236 9680: contig of 1445 bp in length
 * 9681 9781: gap of unknown length
 * 9782 10866: contig of 1086 bp in length
 * 10867 10966: gap of unknown length
 * 10967 12755: contig of 1789 bp in length
 * 12756 12855: gap of unknown length
 * 12856 14226: contig of 1371 bp in length
 * 14227 14326: gap of unknown length
 * 14327 15527: contig of 1201 bp in length
 * 15528 15627: gap of unknown length
 * 15628 16668: contig of 1041 bp in length
 * 16669 16768: gap of unknown length
 * 16769 18505: contig of 1737 bp in length
 * 18506 18605: gap of unknown length
 * 18606 19771: contig of 1166 bp in length
 * 19772 19871: gap of unknown length
 * 19872 20954: contig of 1083 bp in length
 * 20955 21054: gap of unknown length
 * 21055 23215: contig of 2161 bp in length
 * 23216 24700: contig of 1385 bp in length
 * 24701 24800: gap of unknown length

24801 25986: contig of 1186 bp in length
 * 25987 26086: gap of unknown length
 * 26087 27632: contig of 1546 bp in length
 * 27633 27732: gap of unknown length
 * 27733 29722: contig of 1989 bp in length
 * 29723 29821: gap of unknown length
 * 29822 31292: contig of 1470 bp in length
 * 31293 31391: gap of unknown length
 * 31392 33459: contig of 2068 bp in length
 * 33460 33559: gap of unknown length
 * 33560 34894: contig of 1335 bp in length
 * 34895 34994: gap of unknown length
 * 34995 36115: contig of 1121 bp in length
 * 36116 36215: gap of unknown length
 * 36216 37967: contig of 1752 bp in length
 * 37968 38067: gap of unknown length
 * 38068 40967: gap of unknown length
 * 40968 42700: contig of 1733 bp in length
 * 42701 42800: gap of unknown length
 * 42801 45131: contig of 2311 bp in length
 * 45132 45231: gap of unknown length
 * 45232 48268: contig of 3037 bp in length
 * 48269 48368: gap of unknown length
 * 48369 50510: contig of 2142 bp in length
 * 50511 50610: gap of unknown length
 * 50611 52606: contig of 1996 bp in length
 * 52607 52706: gap of unknown length
 * 52707 55721: contig of 3015 bp in length
 * 55722 57821: gap of unknown length
 * 57822 54909: contig of 2588 bp in length
 * 54910 58509: gap of unknown length
 * 58510 61633: contig of 3123 bp in length
 * 61634 61732: gap of unknown length
 * 61733 64083: contig of 2357 bp in length
 * 64084 64183: gap of unknown length
 * 64184 66634: contig of 2445 bp in length
 * 66635 66734: gap of unknown length
 * 66735 69819: contig of 3085 bp in length
 * 69820 69919: gap of unknown length
 * 69920 72225: contig of 2305 bp in length
 * 72226 72324: gap of unknown length
 * 72325 72325: contig of 3117 bp in length
 * 72326 75641: gap of unknown length
 * 75642 77942: contig of 2244 bp in length
 * 77943 78085: gap of unknown length
 * 78086 80809: contig of 2724 bp in length
 * 80810 80909: gap of unknown length
 * 80910 81009: contig of 2191 bp in length
 * 81010 83200: gap of unknown length
 * 83201 86457: contig of 3257 bp in length
 * 86458 86557: gap of unknown length
 * 86558 87618: contig of 1261 bp in length
 * 87619 89718: gap of unknown length
 * 89719 92388: contig of 2670 bp in length
 * 92389 92488: gap of unknown length
 * 92489 94059: contig of 1571 bp in length
 * 94060 94159: gap of unknown length
 * 94160 97600: contig of 3341 bp in length
 * 97601 100407: gap of unknown length
 * 100408 100507: contig of 2807 bp in length
 * 100508 103939: contig of 3432 bp in length
 * 103940 104039: gap of unknown length
 * 104040 106122: contig of 4273 bp in length
 * 106123 108413: gap of unknown length
 * 108414 112121: contig of 3709 bp in length
 * 112122 112221: gap of unknown length
 * 112222 115704: contig of 3483 bp in length
 * 115705 115804: gap of unknown length
 * 115805 122058: contig of 6254 bp in length
 * 122059 122158: gap of unknown length
 * 122159 126727: contig of 4569 bp in length

* 126728 126927: gap of unknown length

Query Match 73.8% Score 19.21 DB 9: Length 156012;
Best Local Similarity 87.5% Fred No. 2.6e+02;
Matches 21: Conserved 0: Mismatches 1: Indels 0: Gaps 0:

QY 1 GAGTAAATCTTCTCTGACCA 24
|||||
DB 100928 GTGACAACTTCTCTGACCA 100951

RESULT 12

AC002422 160091 bp DNA linear PRI 30-JAN-1998
Human Chromosome X, complete sequence.

AC002422.1 GI:2826450
HTG.

SOURCE

Homo sapiens
Bokaryof; Metazoa; Chordata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

1 (bases 1 to 160091)
Chen E., Brownstein, H.H., Stiles, D.J., Schlessinger, D. and
Mazzarella, R.
Direct Submission
Unpublished (1997)
2 (bases 1 to 160091)
Brownstein, H.H., Stiles, D.J. and Mazzarella, R.
Direct Submission
Submitted (12-AUG-1997) Center for Genetics in Medicine, Box 8232,
Washington University School of Medicine, 4566 Scott Avenue, St.
Louis, MO 63110, USA

JOURNAL

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

On Jan 30 1998, this sequence version replaced g1.273237.
Current status of this project is available at:
<http://www.ncbi.nlm.nih.gov/RefSeq/RefSeq.cgi>
Submitted by:
Ellison Chen,
Advanced Center for Genetic Technology,
Applied Biosystems Division of Perkin Elmer Corp.,
850 Lincoln Center Drive,
Foster City, CA 94404 USA
e-mail: ellison@perkin-elmer.com

and

Buddy Brownstein,
Center for Genetics in Medicine,
Washington University School of Medicine, Box 8232,
4566 Scott Avenue,
St. Louis, MO 63110, USA
e-mail: buddy@genetics.wustl.edu

and

David T. Stiles,
Institute for Biomedical Computing
Washington University in St. Louis
700 South Euclid Ave.,
St. Louis, MO 63108 USA
e-mail: stiles@bcmi.wustl.edu,
tostiles@wustl.edu

FEATURES

SOURCE

1. 160091
/organism="Homo sapiens"

BASE COUNT

49262 a 29565 c 30257 g 51067 t

ORIGIN

Query Match 73.8% Score 19.21 DB 9: Length 160091;
Best Local Similarity 87.5% Fred No. 2.6e+02;
Matches 21: Conserved 0: Mismatches 1: Indels 0: Gaps 0:

QY 1 GAGTAAATCTTCTCTGACCA 24
|||||
DB 88522 GTGCTAAATTTCTCTGACCA 88545

RESULT 13

AL592546 174776 bp DNA linear PRI 15 Nov 2001
Human DNA sequence from clone RP11-211N11 on chromosome 10,
complete sequence.

AL592546
AL592546.7 GI:15591647
HTG.

SOURCE

Homo sapiens
Bokaryof; Metazoa; Chordata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

1 (bases 1 to 174776)
Bird, C.
Direct Submission
Submitted (15 NOV 2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humgen@sanger.ac.uk; sanger@hinxton.ac.uk
On Sep 12, 2001 this sequence version replaced g1.15041956.
Sorting sequence assembly data is completed from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

COMMENT

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >
10); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: EMBL, EMBL; SWISSPROT, SWISSPROT; TrEMBL, TrEMBL; WORMBASE, information on the WORMBASE
database can be found at
<http://www.sanger.ac.uk/ftp/seq/seq.html>. This sequence
was generated from part of bacterial clone contigs of human
chromosome 10, contributed by the Sanger Centre chromosome 10
Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/ftp/seq/seq.html>
RP11-211N11 is from the library RP11-1 constructed by the group
of Peter de Jong. For further details see
<http://www.sanger.ac.uk/ftp/seq/seq.html>
Vector: pBlue-script

FEATURES

SOURCE

1. 174776
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-211N11"
/clone_lib="RP11-1"

BASE COUNT 51535 a 35292 c 35407 g 42542 t

ORIGIN

Query Match 73.8% Score 19.21 DB 9: Length 174776;
Best Local Similarity 87.5% Fred No. 2.6e+02;
Matches 21: Conserved 0: Mismatches 1: Indels 0: Gaps 0:

QY 1 GTGCTAAATCTTCTCTGACCA 24
|||||

DB 109754 GTGACAACTTCTCTGACCA 109731

RESULT 14
AC129388
LOCUS
DEFINITION
AC129388 18757 bp. DNA linear 110620 29 JUL 2002
Rattus norvegicus clone CH230 308, *** Sequencing in progress ***
65 unordered pieces.
AC129388
AC129388.1 31,220,1459
http://hrc.phnsl.org
Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 187357)
Muzny, D.M., Adams, C., Adio-Oduola, B., All-ouman, F.R., Allen, C.,
Alsbrooks, S.J., Amaral, H.C., Are, J.R., Ayala, M., Banks, T.,
Barbieri, J., Beutler, J., Bimaye, K., Blackenburg, K., Bonin, L.,
Bouck, J., Bowe, S., Brice, M., Brown, E., Brown, M., Bryant, L.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.E., Carter, M., Cavazos, S.F., Chacko, J., Clavel, D.,
Cleveland, C.D., Clev, C., Clev, M.F., Cuthbert, S.F., David, R.,
David, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
DeLaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Donthawale, K.T., Draper, H., Dugan-Moore, S., Durbin, K.J.,
Earhart, C., Edgar, D., Edwards, C.C., Elhal, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Fratitz, P.,
Gabel, A., Gao, J., Garcia, A., Garmon, T., Garza, N., Gill, P.,
Gorrell, J.H., Guevara, M., Gunatille, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, J., Howard, A., Hughes, M., Hui, Y., Hume, T., Jackson, L.E.,
Jensen, F., Jensen, S., Jeter, T., Joly, S., Joly, T., Johnson, R.,
Johnson, R., Jia, Y., Johnson, R., Joly, S., Joly, T., Johnson, R.,
Karlsson, R., Kelly, S., Khan, U., Ning, L., Korvath, J., Kovar, C.,
Kritov, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.,
Li, J., Li, Z., Lichstein, O., Liu, C., Liu, J., Liu, W., Loughgheed, H.,
Lozano, R., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapa, F., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mel, G., Metzger, M.,
Miner, C., Miner, C., Mitchell, T., Molabadi, K., Morgan, M., Morris, S.,
Mosier, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, R., Nwokwesi, S., Ogih, M., Okuyama, G.,
Oguyama, N., Owens, P., Page, A., Payton, B., Perry, T., Perry, T.,
Peters, L., Pickett, R., Primus, E., Pu, L., Quiles, M., Ren, Y.,
Rivers, M., Rojas, A., Roubekam, I., Rolfe, M., Ruiz, S., Savary, G.,
Schmitt, S., Shi, G., Shi, R., Shrestha, N., Sisson, L.,
Sodergren, P., Sonejko, F., Sparks, A., Stanley, H., Stone, M.,
Sutton, A., Svalok, A., Taber, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansley, J., Taylor, C., Taylor, T., Telford, R., Thomas, N., Thomas, S.,
Usmani, K., Vazquez, L., Vera, V., Villalón, P., Vinson, P., Wolf, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S.,
Williams, C., Williamson, A., Wlodek, P., Wlodan, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y., Zhou, J., Zarrillo, S., Nelson, D.,
Weinstock, G., and Gibbs, R.
TITLE
JOURNAL
REFERENCE
AUTHORS
TITL
JOURNAL
COMMENT
Submitted (29-Jul-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: gky
Center clone name: CH230-9G8
Summary Statistics

Sequencing vector: Plasmid.
Chemistry: Dye terminator Big Dye 3.008 of reads
(see http://www.laservision.com/edu/edu/genbank/draft_data.html).
Assembly program: Phrap; version 0.940329
Consensus quality: 139705 bases at least Q40
Consensus quality: 14615 bases at least Q30
Consensus quality: 15361 bases at least Q20
NOTE: Estimated insert size may differ from sequence length
NOTE: This is a "working draft" sequence. It currently
consists of 65 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
1 1046: contig of 1046 bp in length
1047 1146: gap of unknown length
1147 1340: contig of 194 bp in length
1340 2241 3340: gap of unknown length
2241 2341 3564: contig of 1224 bp in length
2341 3564 3665: gap of unknown length
3564 3665 4820: contig of 1156 bp in length
3665 4820 4921 5965: gap of unknown length
4820 4921 5965: contig of 1045 bp in length
5965 6066 7098: gap of unknown length
6066 7098 7198: contig of 1033 bp in length
7098 7198 8393: gap of unknown length
7198 8393 8490: contig of 1192 bp in length
8393 8490 10491: gap of unknown length
8490 10491 10592: contig of 2001 bp in length
10491 10592 12310 13309: gap of unknown length
10592 12310 12409: contig of 1718 bp in length
12310 12409 13757: gap of unknown length
12409 13757 13856: contig of 1347 bp in length
13757 13856 16066: gap of unknown length
13856 16066 16165: contig of 2209 bp in length
16066 16165 17870: gap of unknown length
16165 17870 17970: contig of 1705 bp in length
17870 17970 17971 18832: gap of unknown length
17971 18832 19933: contig of 1662 bp in length
18832 19933 21542: gap of unknown length
19933 21542 21643: contig of 1619 bp in length
21542 21643 23454: gap of unknown length
21643 23454 23554: contig of 1812 bp in length
23454 23554 25222: gap of unknown length
23554 25222 25723: contig of 1668 bp in length
25222 25723 27173: gap of unknown length
25723 27173 27274: contig of 1851 bp in length
27173 27274 28660: gap of unknown length
27274 28660 28760: contig of 1387 bp in length
28660 28760 30021 30121: gap of unknown length
28760 30021 30121: contig of 1261 bp in length
30021 30121 31325: gap of unknown length
30121 31325 31425: contig of 1204 bp in length
31325 31425 32887: gap of unknown length
31425 32887 32987: contig of 1462 bp in length
32887 32987 34739: gap of unknown length
32987 34739 34839: contig of 1752 bp in length
34739 34839 36695: gap of unknown length
34839 36695 36795: contig of 1856 bp in length
36695 36795 39280: gap of unknown length
36795 39280 39380: contig of 2485 bp in length
39280 39380 40710: gap of unknown length
39380 40710 40711 42192: gap of unknown length
40711 42192 42193: contig of 1330 bp in length
42193 42194 42593: gap of unknown length
42194 42593 44372: contig of 1682 bp in length
42593 44372 44373: gap of unknown length
44373 45946: contig of 1680 bp in length
44373 45946 45947 46046: contig of 1574 bp in length
45947 46046: gap of unknown length

Sequencing Vector: Plasmid:

Chemistry: Dye-terminator Big Dye 100% of reads

Assembly program: Phrap; version 0.993329

Consensus quality: 96813 bases at least Q40

Consensus quality: 103408 bases at least Q30

Consensus quality: 107911 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length.

* (see <http://www.blast.lanl.gov/blast/blast.cgi?seqs=us09-910-428-1.rge>)

* NOTE: This is a 'working draft' sequence. It currently

* consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 1664: contig of 1664 bp in length

* 1665 1764: gap of unknown length

* 1765 3115: contig of 1351 bp in length

* 3116 4220: gap of unknown length

* 4221 4320: contig of 1005 bp in length

* 4321 5450: contig of 1130 bp in length

* 5451 5550: gap of unknown length

* 5551 6821: contig of 1271 bp in length

* 6822 8321: gap of unknown length

* 8322 8421: contig of 100 bp in length

* 8422 9412: gap of unknown length

* 9413 10798: contig of 1186 bp in length

* 10799 12339: gap of unknown length

* 12340 13339: contig of 1341 bp in length

* 13340 14340: gap of unknown length

* 14341 14860: contig of 1401 bp in length

* 14861 14960: gap of unknown length

* 14961 16572: contig of 1612 bp in length

* 16573 16672: gap of unknown length

* 16673 17551: contig of 1079 bp in length

* 17552 17851: gap of unknown length

* 17852 19156: contig of 1305 bp in length

* 19157 19256: gap of unknown length

* 19257 20442: contig of 1186 bp in length

* 20443 21730: gap of unknown length

* 21731 21873: contig of 144 bp in length

* 21874 23036: gap of unknown length

* 23037 23136: contig of 1106 bp in length

* 23137 24364: gap of unknown length

* 24365 25865: contig of 1401 bp in length

* 25866 25965: gap of unknown length

* 25966 26967: contig of 1002 bp in length

* 26968 27067: gap of unknown length

* 27068 28402: contig of 1335 bp in length

* 28403 28502: gap of unknown length

* 28503 29580: contig of 1078 bp in length

* 29581 29680: gap of unknown length

* 29681 30688: contig of 1188 bp in length

* 30689 30968: gap of unknown length

* 30969 32178: contig of 1210 bp in length

* 32179 32278: gap of unknown length

* 32279 33363: contig of 1085 bp in length

* 33364 33463: gap of unknown length

* 33464 34925: contig of 1462 bp in length

* 34926 35025: gap of unknown length

* 35026 36257: contig of 1232 bp in length

* 36258 36357: gap of unknown length

* 36358 37973: contig of 1616 bp in length

* 37974 38073: gap of unknown length

* 38074 39321: contig of 1248 bp in length

* 39322 40591: gap of unknown length

* 40592 40691: contig of 1170 bp in length

* 40692 42129: gap of unknown length

* 42130 42229: contig of 1438 bp in length

* 42230 43683: gap of unknown length

* 43684 44220: contig of 1454 bp in length

* 44221 44901: gap of unknown length

* 44902 45001: contig of 1118 bp in length

* 45002 45902: gap of unknown length

* 45903 46727: contig of 1726 bp in length

* 46728 48055: gap of unknown length

* 48056 48165: contig of 1238 bp in length

* 48166 49363: gap of unknown length

* 49364 49463: contig of 1198 bp in length

* 49464 51394: gap of unknown length

* 51395 51494: contig of 1931 bp in length

* 51495 53434: gap of unknown length

* 53435 53534: contig of 1940 bp in length

* 53535 55051: gap of unknown length

* 55052 55151: contig of 1517 bp in length

* 55152 56544: gap of unknown length

* 56545 58125: contig of 1393 bp in length

* 58126 58225: gap of unknown length

* 58226 60333: contig of 1481 bp in length

* 60334 60933: gap of unknown length

* 60934 62340: contig of 1407 bp in length

* 62341 62440: gap of unknown length

* 62441 63742: contig of 2008 bp in length

* 63743 64848: gap of unknown length

* 64849 64948: contig of 1106 bp in length

* 64949 66444: gap of unknown length

* 66445 66544: contig of 1696 bp in length

* 66545 69138: gap of unknown length

* 69139 69238: contig of 2394 bp in length

* 69239 71838: gap of unknown length

* 71839 71938: contig of 2600 bp in length

* 71939 73482: gap of unknown length

* 73483 73582: contig of 1544 bp in length

* 73583 75157: gap of unknown length

* 75158 75257: contig of 1575 bp in length

* 75258 77439: gap of unknown length

* 77440 77539: contig of 2182 bp in length

* 77540 79417: gap of unknown length

* 79418 79517: contig of 1878 bp in length

* 79518 81024: gap of unknown length

* 81025 81124: contig of 1507 bp in length

* 81125 82608: gap of unknown length

* 82609 82608: contig of 1484 bp in length

Query Match:

Best Local Similarity:

Matches 21: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

Query 3 GCGCTAAGCTTCTGCTACGACG 26

Db 74593 GCGCTAAGCTTCTGCTACGACG 74670

Search completed: January 14 2003, 14:04:38
Job time: 383.313 secs

